AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (Currently Amended) A method for analyzing exon expression in a cell sample, comprising measuring the expression levels of a plurality of different individual exons or different individual multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived, wherein at least one gene in said plurality of different genes has an exon having a plurality of different variants, and wherein said ~~measuring~~ method further comprises measuring the expression level of each of said plurality of different variants of said exon in said at least one gene, each of said plurality of different variants being a different splice form of said exon generated using a different 3′ or 5′ splice junction of said exon; thereby analyzing the exon expression of said cell sample.

Claims 2-3 (Canceled).

4. (Previously Presented) The method of claim 1, wherein said plurality of different individual exons or different individual multiexons consists of at least 3 different exons or multiexons.

5. (Previously Presented) The method of claim 1, wherein said plurality of different individual exons or different individual multiexons consists of at least 5 different exons or multiexons.

6. (Previously Presented) The method of claim 1, wherein said plurality of different individual exons or different individual multiexons consists of at least two different exons.

7. (Previously Presented) The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 100 different genes.

8. (Previously Presented) The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 1,000 different genes.

9. (Previously Presented) The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 10,000 different genes.

10. (Previously Presented) The method of claim 1, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample, wherein said plurality of probes comprises probes that allow measurement of the expression levels of said plurality of different variants of said exon; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

11. (Previously Presented) The method of claim 10, wherein said plurality of different individual exons or different individual multiexons consists of at least 3 different exons.

12. (Previously Presented) The method of claim 10, wherein said plurality of different individual exons or different individual multiexons consists of at least 5 different exons.

13. (Previously Presented) The method of claim 10, 11 or 12, wherein said plurality of different genes consists of at least 1,000 different genes.

14. (Previously Presented) The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

15. (Previously Presented) The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

16. (Previously Presented) The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

17. (Previously Presented) The method of claim 10, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

18. (Previously Presented) The method of claim 10, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

19. (Previously Presented) The method of claim 10, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

20. (Previously Presented) The method of claim 10, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

21. (Previously Presented) The method of claim 10, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

22. (Previously Presented) The method of claim 10, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

23. (Previously Presented) The method of claim 10, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

24. (Previously Presented) The method of claim 10, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

25. (Previously Presented) The method of claim 10, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

26. (Previously Presented) The method of claim 10, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

27. (Previously Presented) The method of claim 10, wherein each of said different nucleotide sequences consists of 60 nucleotides.

28. (Previously Presented) The method of claim 10, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

29. (Previously Presented) The method of claim 28, wherein said linker sequence comprises a linker sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

30. (Previously Presented) The method of claim 10, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary to the sequence of a full length exon.

31. (Previously Presented) The method of claim 10, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

32. (Previously Presented) The method of claim 31, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

33. (Previously Presented) The method of claim 31, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

34. (Previously Presented) The method of claim 10, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

35. (Canceled).

36. (Previously Presented) The method of claim 1 or 10, wherein said expression levels are measured as abundance of mRNA transcripts.

Claims 37-44 (Canceled).

45. (Previously Presented) The method of claim 1 or 10, wherein said organism is a human.

46. (Withdrawn) The method of claim 1 or 10, wherein said organism is a plant.

Claims 47-85 (Canceled).

86. (Previously Presented) The method of claim 1 or 10, wherein said cell sample has been subjected to a perturbation.

87. (Previously Presented) The method of claim 86, wherein said organism is a human.

88. (Withdrawn) The method of claim 86, wherein said organism is a plant.

89. (Previously Presented) The method of claim 86, further comprising comparing the expression levels of at least a portion of said plurality of different individual exons or different individual multiexons in said cell sample having been subjected to said perturbation with the expression level of said portion of said plurality of different individual exons or different individual multiexons in a cell sample of the same type not having been subjected to said perturbation.

90. (Previously Presented) The method of claim 89, wherein said comparing comprises determining the difference between the expression level of each exon or multiexon in said portion of said plurality of different individual exons or different individual multiexons in said cell sample having been subjected to said perturbation and the expression level of the corresponding exons or multiexons in said cell sample of the same type not having been subjected to said perturbation.

Claims 91-156 (Canceled).

157. (Previously Presented) The method of claim 1, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived, wherein said plurality of probes comprises probes that allow

measurement of the expression levels of said plurality of different variants of said exon; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

158. (Previously Presented) The method of claim 157, wherein said plurality of different individual exons or different individual multiexons consists of at least 3 different exons.

159. (Previously Presented) The method of claim 157, wherein said plurality of different individual exons or different individual multiexons consists of at least 5 different exons.

160. (Previously Presented) The method of claim 157, 158 or 159, wherein said plurality of different genes consists of at least 1,000 different genes.

161. (Previously Presented) The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

162. (Previously Presented) The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

163. (Previously Presented) The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

164. (Previously Presented) The method of claim 157, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

165. (Previously Presented) The method of claim 157, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

166. (Previously Presented) The method of claim 157, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

167. (Previously Presented) The method of claim 157, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

168. (Previously Presented) The method of claim 157, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

169. (Previously Presented) The method of claim 157, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

170. (Previously Presented) The method of claim 157, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

171. (Previously Presented) The method of claim 157, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

172. (Previously Presented) The method of claim 157, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

173. (Previously Presented) The method of claim 157, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

174. (Previously Presented) The method of claim 157, wherein each of said different nucleotide sequences consists of 60 nucleotides.

175. (Previously Presented) The method of claim 157, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

176. (Previously Presented) The method of claim 175, wherein said linker sequence comprises a spacer sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

177. (Previously Presented) The method of claim 157, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary to the sequence of a full length exon.

178. (Previously Presented) The method of claim 157, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

179. (Previously Presented) The method of claim 178, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

180. (Previously Presented) The method of claim 178, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

181. (Previously Presented) The method of claim 157, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

182. (Canceled).

183. (Previously Presented) The method of claim 157, wherein said expression levels are measured as abundance of mRNA transcripts.

Claims 184-211 (Canceled).

212. (Withdrawn) The method of claim 1 or 10, wherein said organism is a fungus.

213. (Withdrawn) The method of claim 86, wherein said organism is a fungus.

Claims 214-262 (Canceled).

263. (Previously Presented) The method of claim 10 or 157, wherein said array of polynucleotide probes comprises one or more sets of successive overlapping probes tiled along the longest length variant among said plurality of different variants of said exon.

264. (Previously Presented) The method of claim 10 or 157, wherein said array of polynucleotide probes comprises variant junction probes, wherein each of said variant junction probes is specifically hybridizable to a sequence spanning the splice junction

between a different variant of said exon having a plurality of different variants and an adjacent exon.

265. (Previously Presented) The method of claim 86, wherein said perturbation is exposure to a drug.

266. (Withdrawn) The method of claim 86, wherein said perturbation is a genetic mutation.

267. (Withdrawn) The method of claim 86, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.

Claims 268-279 (Canceled).

280. (Previously Presented) The method of claim 32 or 179, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

281. (Previously Presented) The method of claim 280, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

282. (Previously Presented) The method of claim 281, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

283. (Previously Presented) The method of claim 282, wherein each of said different nucleotide sequences consists of 60 nucleotides.

284. (Previously Presented) A method for analyzing exon expression in a cell sample of an organism, comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises (i) one or more exon specific probes comprising different nucleotide sequences for each of a plurality of different genes in the genome of said organism, each of said different nucleotide sequences being complementary and hybridizable to a sequence within a different individual exon; and (ii) a variant junction probe for each of a plurality of different variants of at least one exon, each of said variants being a different

splice form of said exon generated using a different 3′ or 5′ splice junction of said exon, and each of said variant junction probes being a probe specific to a junction region of said variant and an adjacent exon in a multiexon comprising said variant of said exon, each of said exon specific probes and variant junction probes being bound to a different region of a support; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

285. (Previously Presented) A method for analyzing exon expression in a cell sample of an organism, comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of junction specific probes comprising different nucleotide sequences for each of a plurality of different genes in the genome of said organism bound to different regions of a support, each of said different nucleotide sequences being complementary and hybridizable to a sequence spanning a junction region of a multiexon, and wherein said plurality of junction specific probes comprises a variant junction probe for each of a plurality of different variants of at least one exon, each of said variants being a different splice form of said exon generated using a different 3′ or 5′ splice junction of said exon, and each of said variant junction probes being a probe specific to a junction region of said variant and an adjacent exon in a multiexon comprising said variant of said exon; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

286. (Previously Presented) The method of claim 284 or 285, wherein said plurality of different genes consists of at least 100 different genes.

287. (Previously Presented) The method of claim 286, wherein said plurality of different genes consists of at least 1,000 different genes.

288. (Previously Presented) The method of claim 287, wherein said plurality of different genes consists of at least 10,000 different genes.

289. (Previously Presented) The method of claim 284 or 285, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

290. (Previously Presented) The method of claim 289, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

291. (Previously Presented) The method of claim 290, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

292. (Previously Presented) The method of claim 291, wherein each of said different nucleotide sequences consists of 60 nucleotides.

293. (Previously Presented) The method of claim 1, 10 or 157, wherein said method comprises measuring the expression levels of at least 5 different variants in said plurality of different genes.

294. (Previously Presented) The method of claim 293, wherein said method comprises measuring the expression levels of at least 10 different variants in said plurality of different genes.

295. (Previously Presented) The method of claim 294, wherein said method comprises measuring the expression levels of at least 100 different variants in said plurality of different genes.

296. (Previously Presented) The method of claim 295, wherein said method comprises measuring the expression levels of at least 1000 different variants in said plurality of different genes.